

ACACCATTG TCTTCATGTA ACCCCATTAG CTATACCTC TAGTGCAGG AAACCATAGG
 10 20 30 40 50 60

 GCCTAGGTCA CACCATGAGG CTGCNCTTAC AAGTTATGCA AAAACTATGG ACTTGGGAGA
 70 80 90 100 110 120

 CCTGTGCGTA ACAACATCAC ACNCCAAATT TAACCAGCTC TCCCCATAAC AGCACGCTCA
 130 140 150 160 170 180

 TGTGTTACTG AGGAAATGCC TGTGGATTGG AGTGTGTTCT GTGTGCAGGA GGCTGGTCCA
 190 200 210 220 230 240

 GGTTTCACCTT CTGCAGGACA CTGGACGTTT CCCAAAACCA GCAGACTTTC CCCACGTGCA
 250 260 270 280 290 300

 CACACACCCC TTCTCATTTT GCCTCTACAT CCATATCCAC TGGGCCCTTC AGGCACCTAC
 310 320 330 340 350 360

 TAATGCCCTA GAACCTAAAA CCATCATCTG GGGCCCAGTT CCCTGAATGG CCCTAACCTC
 370 380 390 400 410 420

 TTCCTCTGCT GGAATGAGTC CAGTGCCAC TTCCCTCAAAC GGTGAAATTG CTGGGCTGCT
 430 440 450 460 470 480

 ACAGATCAGG AACTCACTGC TTCCCTCATAG GGGCAGCCGA CTTCACTGCT CTGCAACAGC
 490 500 510 520 530 540

 GACCACCCCT AGCGAGGCTT GAGATGCCCT TTGCCTCCCTT AAGACTGAGG GAGACGCTTC
 550 560 570 580 590 600

 AGCTCTCACT CCACTGCCCT AAGTCCTCCA CAGCGCGGTG CCTGCTGCCT TCACACAGAG
 610 620 630 640 650 660

 CTGCAGGGGN AGGTCCCTGT TATCCGGCCT GCTGGACCAG CGCTGTGCAC AACCCCTCCCA
 670 680 690 700 710 720

 TGGCAACAGT GGCTGCCCGG CCTGCACACT GGGCTTGGCA ACCTCGCTGT AGGTATTTAT
 730 740 750 760 770 780

 TCCCTCAGGA GTGACTGCAT TCTTTTCCCA TTTCCAGAAA ACTGATGCCA TTTACCTCAC
 790 800 810 820 830 840

 TATGAGGGAGG AGGAGGGAGGA GGAGGGTGGA GAGTGGTACA TTTTAAAATG TGCACATTTC
 850 860 870 880 890 900

 TCCCTAGGAC TCCCCCTCAA ATAACCCAGG AGGGACCATA CCAGCTCATT CCTGTGTATC
 910 920 930 940 950 960

 CCAAGCATAN GAGTAATCAT CCCACTCATG CTGAGTGTAT GGTGGCCATT AAGCCTGCC
 970 980 990 1000 1010 1020

Figure 1

PROMOTER REGION

TGAACTGGCT	TTAGAACAAAG	GTGTTGAGC	ACACAGCACC	GTCTTGCTGC	CACCTTGGCC
1030	1040	1050	1060	1070	1080
CCCTCCCTTG	TGAGACCTCT	GAGACACATT	NAGGTCTCAC	CTAAAATCT	CAGGATTCT
1090	1100	1110	1120	1130	1140
AGGCCCAAAN	CGGTCTAA	AAATTGTTCA	GTCTGAACTC	TCTAAGGTCA	AGAGAAGAGG
1150	1160	1170	1180	1190	1200
TGGTTGCTCC	CTCTAAAGAAA	CCACATGTTG	CATGTACATC	CTTAATTCCG	GAAAGTCCAA
1210	1220	1230	1240	1250	1260
CAAACCTGCC	CTGCTTAGCA	ACACAAGCCG	AGGTGGTACT	CCTCTCACCC	GGGCATTCTC
1270	1280	1290	1300	1310	1320
CAACACACCT	GTTTGTCCAA	ACAGCTTGA	TTTGTGTTTA	TAGTTGGACC	CCAGGTTCCC
1330	1340	1350	1360	1370	1380
AGGAGGCTGG	TTCAGGCCAT	ATTCCAAATC	CTCATCTGTG	TGTGAGTGGC	ATTCTTAGCC
1390	1400	1410	1420	1430	1440
TAGCCTCCTT	ACAGGGTGG	TACTATGATA	CACAGCCAGG	CTGTCCAGT	GGCTTTCAAT
1450	1460	1470	1480	1490	1500
ATTCTTTGG	TCCAGATAGT	TCAGCCTCAG	CACCAGTGTA	GGCATCACAG	GGTCAATTGT
1510	1520	1530	1540	1550	1560
CTTAGGAGTC	ATGGAGAATT	CATAGTTGGT	AGCTACCTGG	GCCTGGCCAG	GGCTGACCAC
1570	1580	1590	1600	1610	1620
AGACAAGGCA	TCCCTCTGTG	AACTCCTATT	TTAATGCCAG	CTTCCCAACA	AATTTCTCAA
1630	1640	1650	1660	1670	1680
CAAT box					
CTGCTCTTAC	CAGCAGGTAT	TTAAACTACT	CAATAGAAAG	TAACCCTGAA	AATTAGGACA
1690	1700	1710	1720	1730	1740
TATA box					
CCTGTTCCA	AAAGACCCTT	AAATAGGGGA	AGTCCTTCN	CTGCTTGTC	ACAGCTGCTG
1750	1760	1770	1780	1790	1800
->mRNA -----					
ATGTGGCAAC	ATGAGGCCTG	GGACAGGGGA	CTGCTCTCTG	CCCACCTCTGG	TAGCCTCACG
1810	1820	1830	1840	1850	1860
Spsite					
-- exon 1	----->#####				
TAGCTTAACA	ATCTGTCAGT	AATACAATAC	AAAACCTAAA	CTTCATACT	GCGGTTCCAC
1870	1880	1890	1900	1910	1920
CCAGGAAGCT	GTGTTCCCAA	TCTGACCCGT	GATTATGGGG	CCACCTCAGA	GGGNACCCAG
1930	1940	1950	1960	1970	1980

Figure 1 (continued)

TGAGGGAATA TTTTGCCATC TGGGACTGTT GGTTGCTGGG GGCAGTGGCT ATGAGCTCAG
 1990 2000 2010 2020 2030 2040

 TTAATAAACT CAAGCAGTTT CCTTCCAAAC ACACATGTCC TACTAACGT GTCCAACAGA
 2050 2060 2070 2080 2090 2100

 GATGATCATA CTCATANGCT GCTAAAACAT TANTTTTATT TTGAGAAAAG TCTATTGATG
 2110 2120 2130 2140 2150 2160
 ----- Alu insert -----
 TTCTTGGCCC ATGGAGTTT CATTNATTAA NTTTATTTAT TTTGCAGAGA TGGAGTCTCA
 2170 2180 2190 2200 2210 2220

 CTATGTTGCT CAAGCTGGTC TCCAACTCCT GGGCTCAAGC GATCTTCCTA CTTTGGCCTT
 2230 2240 2250 2260 2270 2280

 TGAAAGCGCT GAGATTGCCT GTGTGAGCCA TCATGGGGGC TCACTGGCCC ACTGATTAAT
 2290 2300 2310 2320 2330 2340

 CAGATTAATT GTTTTTGCT ATTGAANTTG TTTGACTTCC TTGTATATTG GGATATTTAC
 2350 2360 2370 2380 2390 2400

 CCATTCTAAC ACGTAGGGTT TGCAAATATT TTCTCTCATG TTCTGTGTTG CCTTTCACT
 2410 2420 2430 2440 2450 2460

 CAGTTGATGG TTTCCTTGCG TGTGCAGGTG CTTTAGTGTG AAACGCAGCC CCGCTTGTCT
 2470 2480 2490 2500 2510 2520

 ATTTTCCATT TTATTGCCTG TCCCTTTGAT GTCATAGCCA AGAAATAATT GCCCAGATTA
 2530 2540 2550 2560 2570 2580

 ATGTCAAAAA GCTTTATCCC TATATATTCT TCTAGTAGTT TATGGTTCA GATCTTATGT
 2590 2600 2610 2620 2630 2640

 TTAGGTCTTC AATCCATTGA GTTGATTTT GTATGTGGTA TAAGAAAAAA GACCACATGT
 2650 2660 2670 2680 2690 2700

 ATACATATCT CAAATTCTAA GGTAGTATAT ATTAGACACA TACAATGTGT CTATTTACAC
 2710 2720 2730 2740 2750 2760

 ACATTGAGCT GAAAATAATA AACATATTTT TATCTTCAA TCAACTCTAT CTCTATCTCA
 2770 2780 2790 2800 2810 2820

 CTGAACTTGT TTCACCTATA GCCTGATGAG GTTGCTGTCC TCTCTACCCC AGCTCCTATA
 2830 2840 2850 2860 2870 2880

 GGAGACTGCT CATCCCCCTAA CCTCAAAAAC CCCTTCATGA GGGTGATAAT GCCCTTGAAT
 2890 2900 2910 2920 2930 2940

Figure 1 (continued)

CCTGCAATGA ATTAGTTCTC TACTACAGTG GAATTCAAGGT CTGTTATGAG GGTCTGGATC
 2950 2960 2970 2980 2990 3000

TCTGAAGAGA AGAGCTCTCA TTTTCAGAAA ATAAGCAGGA TTTATTCCCT GAAATTACTG
 3010 3020 3030 3040 3050 3060

AATTAATCA CTGTTTCGAT TACTTTTGC AATATTAAAA GTAAATATTT AACACAGGTAA
 3070 3080 3090 3100 3110 3120

AAACAGAAAT AATGGTAGGG TCCTTATCAT CACCGTGAAT TCCAAGCTAG CATAGACACT
 3130 3140 3150 3160 3170 3180

AAACCTAGAG ATTCACACTA GAATGAAAGC TGGGAGAGCA GAGGAGTCTC AGAAGGATGT
 3190 3200 3210 3220 3230 3240

GGAGGCCAAT GGACACCTGC AACCTCTCCA ACGAAATGCC TACCTCCTCT CACTGCAGCA
 3250 3260 3270 3280 3290 3300

TCCATCTCTG AGCCTTCTCG CAGCAGAGCT ATAAATTCAG CCTGGCTCCT CCGTTCCCAC
 3310 3320 3330 3340 3350 3360

Spsite CDS start
 #####-----***-----

ACATCCACTC CTGCTCTCCC TCCTCTCCTC CAGGTGACTA CAGTTATGAG GACCCTCAC
 3370 3380 3390 3400 3410 3420

----- Exon 2 -----
 CTCCTCTCTG CCTTTCTCCT GGTGGCCCTT CAGGCCTGGG CAGAGCCGCT CCAGGCAAGA
 3430 3440 3450 3460 3470 3480

 GCTCATGAGA TGCCAGCCCA GAAGCAGCCT CCAGCAGATG ACCAGGATGT GGTCAATTAC
 3490 3500 3510 3520 3530 3540

Spsite
 ----->##### ####

TTTCAGGAG ATGACAGCTG CTCTCTTCAG GTTCCAGGTG AGAGATGCCA GCATGCAGAG
 3550 3560 3570 3580 3590 3600

CTACAGACTA GACAGAAGGA CAGGAGACAG GCTCTGGAAT TGGATCTCAG TGGCAGATGT
 3610 3620 3630 3640 3650 3660

CACTTAGGTG GCTATACTTA ACATCTCTGG TCCTGGATT TCTCATATCT AAATGGAATA
 3670 3680 3690 3700 3710 3720

GAGAACCAAA GAAATCTAAG AGATTTTCT TTCTCCAAAA ACTTGATTCC AAGATATGAC
 3730 3740 3750 3760 3770 3780

TGTGAAATTCA ACTAGATTAA AGATATAAGG AGATGCTACC TAGTTCTTC TGGAGCCAGA
 3790 3800 3810 3820 3830 3840

Figure 1 (continued)

CAAACAAGCT TAAGTATATA GGAAAATATT TCACCCCTGTC TATATAGGAG GTTTTAGAAC
 3850 3860 3870 3880 3890 3900

CTGGAGAGGA GCCTAAGAAT GTGTTCAGGT GTGTGTGTGA TGGGCAGGAA TGCAGAAAAG
 3910 3920 3930 3940 3950 3960

TGAAGCAAAG GAGAATGAGT CTCGAATCCT GTGTGACCAAG CACTGCTCTG TGTATTTATT
 3970 3980 3990 4000 4010 4020

CCTATTGACT GAGATTGTTT GTGCTACCGG CTGTAATACA GCCAACATCA CTCATCAGCC
 4030 4040 4050 4060 4070 4080

AACATGTGAC TTCTCCAAGA TTCCCTTTAC CACCCACTGC TGNACCCCGT ACTCAGTTTC
 4090 4100 4110 4120 4130 4140

Spsite

<-----

TGATGCTCTC TCTGGGTCCC CAGGCTCAAC AAAGGGCTTG ATCTGCCATT GCAGAGTACT
 4150 4160 4170 4180 4190 4200

----- Exon 3 -----

ATACTGCATT TTTGGAGAAC ATCTTGGTGG GACCTGCTTC ATCCTTGGTG AACGCTACCC
 4210 4220 4230 4240 4250 4260

CDS stop

***-----

AATCTGCTGC TACTAAGCTT GCAGACTAGA GAAAAAGAGT TCATAATTTC CTTTGAGCAT
 4270 4280 4290 4300 4310 4320

Poly Ad

*****----->

TAAAGGGAAT TGTTATTCTT ATACCTTGTC CTCGATTCC TGTCTCATC CCAAATAAAT
 4330 4340 4350 4360 4370 4380

ACTTGGTAAC ATGATTTCCG GGTTTTTTTT TTTTT
 4390 4400 4410

Figure 1(continued)

	10	20	30	40	50		
DEF4	GGATCCCCATTGTCTCAGTGTAAACCC-ATTAGTTAACCGCCTACTGCAAGGAAACCA						
DEFX	ACACCATTGTCTTCAGTGTAAACCCATTAGCTATACCCCTCTAGTGCAAGGAAACCA						
	10	20	30	40	50		
	60	70	80	90	100	110	
DEF4	CAAGGCTTGGATCAGATCATGAGGCTGCCCT-ACAAGTTATGCCAAAAAATATGGACTTG						
DEFX	TAGGGCCTAGGTACACCATGAGGCTGCNCTTACAAGTTATGC-AAAAACTATGGACTTG						
	60	70	80	90	100	110	
	120	130	140	150	160	170	
DEF4	GAAGACCTGTCTGTATAATATCACAC-CCAAATCTAACAGCTCTGCCAATAACAGCTC						
DEFX	GGAGACCTGTGCGTAACAACATCACACNCACAAATTAAACCAGCTCTCCCATAACAGCAC						
	120	130	140	150	160	170	
	180	190	200	210	220	230	
DEF4	TCTCCTATGTTACTAGGAAAATGCCTATGGATTGGAGTGTGTTCTGTGTCAGGAGGCTG						
DEFX	GCTCATGTTACTGAGGAAATGCCTGTGGATTGGAGTGTGTTCTGTGTCAGGAGGCTG						
	180	190	200	210	220	230	
	240	250	260	270	280	290	
DEF4	GTCCAGGTTTCACTTCTGCAGGACACTGGACATC-CCCACAACCACAGACCTTCCCCAC						
DEFX	GTCCAGGTTTCACTTCTGCAGGACACTGGACGTTCCAAAACCAGCAGACTTTCCCCAC						
	240	250	260	270	280	290	
	300	310	320	330	340	350	
DEF4	GTGCACACACACCCCTCTCATTTGCCTCTACATCCATATCCACTGGGCCCTCAGGCA						
DEFX	GTGCACACACACCCCTCTCATTTGCCTCTACATCCATATCCACTGGGCCCTCAGGCA						
	300	310	320	330	340	350	
	360	370	380	390	400	410	
DEF4	CCTACTAATGCCCTAGAACCTAAACCATCATCTGGGGCCAGTTCCCCAAATAGGCCCTA						
DEFX	CCTACTAATGCCCTAGAACCTAAACCATCATCTGGGGCCAGTTCCCTGAATGCCCTA						
	360	370	380	390	400	410	
	420	430	440	450	460	470	
DEF4	ATTTCTTCTCTGCTGGAATGAGTCCAGTGCCACTTCTCCAAAGGTGAAATTGCTGGG						
DEFX	ATCTCTTCTCTGCTGGAATGAGTCCAGTGCCACTTCTCCAAACGGTGAAATTGCTGGG						
	420	430	440	450	460	470	
	480	490	500	510	520	530	
DEF4	CCTGCAACAGATCAGGAACACTGCTTC-TCATAGGGCAGCCGACTTCAGTGCTCTGG						
DEFX	C-TGCTACAGATCAGGAACACTGCTTCAGTGCTCTGG						
	480	490	500	510	520	530	

Figure 2

	540	550	560	570	580	590
DEF4	AACAGCGACCACCCCTAGCGAGGCTTGAGATGCCTCTTCCCTCCTTAAGACTGAGAGCGC					
DEFX	::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::					
	540	550	560	570	580	590
	600	610	620	630		
DEF4	CGCT-----GCCCGAGTCCTCCATAGCCCAGTGCCTGGCTGCCTTCA					
DEFX	::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::					
	600	610	620	630	640	650
	640	650	660	670	680	690
DEF4	GCCAGAGCTGCAGGGG-AGGCCCTGAGCACCCAAGTCCTGCTGGACCAGCGCTGTGCACG					
DEFX	::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::					
	660	670	680	690	700	710
	700	710	720	730	740	750
DEF4	GCCCTCCCATGGCGGCAGGGCTGCCTGGACTGCATACTGGGTTAGCAACCTCACTATA					
DEFX	::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::					
	720	730	740	750	760	770
	760	770	780	790	800	810
DEF4	GGTATTCTCCCTCAGGAACAATGCATTCTTCTCATTCCAGAAACCTCATCCCGT					
DEFX	::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::					
	780	790	800	810	820	830
	820	830	840	850	860	
DEF4	TTACCTCACTACAAGGAGGAGGATG-----GTGGAGAGTGGTACATTTAAAATGT					
DEFX	::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::					
	840	850	860	870	880	890
	870	880	890	900	910	920
DEF4	GCACTAGTCTCCCTGGACTCCCCCTCAAATAACCCAGGAGGGACCACACAAGGGAAAGC					
DEFX	::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::					
	900	910	920	930	940	950
	930	940	950	960	970	980
DEF4	TTATGCATCCCCCCCACCC-AGTGACCATCTCCTAACTCTGGGTGTAGGGAGACTCGTA					
DEFX	::: ::::: ::: . ::: : ::: : ::: : ::: : ::: : ::: :::					
	960	970	980	990	1000	1010
	990	1000	1010	1020	1030	1040
DEF4	AGCCTACG--GGATTGGTTGGAACAGGGTATTTGAGCTCACACACAGGTGATGCAA					
DEFX	::::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::					
	1020	1030	1040	1050	1060	

Figure 2 (continued)

TGCCTGCGATGAGGAAACACATGTT

	1050	1060	1070	1080	1090	1100
DEF4	GCTAACACCAATCTCGCTGCAGCTTGCCACCCTTAAGG-GACTTCTGACAGACATT ::: :::: : :: : :: : :: : :: : :: :					
DEFX	-----TCTTGCTGCCACCTGGCCCCCTCCCTGTGAGACCTCTGAGACACATT 1070 1080 1090 1100 1110					
	1110	1120	1130	1140	1150	1160
DEF4	-AGGTGTCACGCAATCATTGATGAGTCCTGGCCTGGAT--GACCTAGACAGTCATTTA ::: :::: : :: : :: : :: : :: : :: :					
DEFX	NAGGTCTCACCTAAAAATCTCAGGATTCTAGGCCAAANCGTCCTAAAAATTGTTCA 1120 1130 1140 1150 1160 1170					
	1170	1180	1190	1200	1210	1220
DEF4	GGCTTGAACATATCTAAGGCCAAGCAAAAGGTGACTGTCCCCTCTAGGAA-CCACATGCT ::: :::: : :::: : :: : :: : :: : :: : :: :					
DEFX	GTCT-GAACTCTCTAAGGTCAAGAGAAGAGGTGGTCTCCCTCTAAGAAACCACATGTT 1180 1190 1200 1210 1220					
	1230	1240	1250	1260	1270	
DEF4	ATATGCACATCCTTACTCGGGAGCCTGCAAC---CTGCCCTATCCAGCAACACAAGCC ::: :::: : :: : :: : :: : :: :					
DEFX	GCATGTACATCCTTAATTCCGGAAAGTCCAACAAACCTGCCCTGCTTAGCAACACACAAGCC 1230 1240 1250 1260 1270 1280					
	1280	1290	1300	1310	1320	1330
DEF4	CAGGCG-TATTCAGTCTCATCCAGGTATTCTCAAC---CTTACTTGTCTGAATGGCTTG ::: : :: : :: : :: : :: : :: : :: :					
DEFX	GAGGTGGTACTCC-TCTCACCCGGGCATTCTCAACACACCTGTTGTCAAACAGCTTT 1290 1300 1310 1320 1330 1340					
	1340	1350	1360	1370	1380	1390
DEF4	GATTTTTTATGGTAGACCCCAGGG-CCTGGGAGGTCAAGTCAGACCACATTCCAAA ::: :::: : :: : :: : :: : :: : :: :					
DEFX	GATTTTTTATAGTTGGACCCCAGGTTCCCAAGGAGGCTGGTTCAGGCCATTCCAAA 1350 1360 1370 1380 1390 1400					
	1400	1410	1420	1430	1440	1450
DEF4	TCCTCATCTGTGTGGGTGGCATTTGATCCTAGTCTCCTCGCAAGGTGTATAACACAA ::: :::: : :: : :: : :: : :: : :					
DEFX	TCCTCATCTGTGTGGTAGTGGCATTCTTAGCCTAGCCTTACAGGGTGGATACTATGA 1410 1420 1430 1440 1450 1460					
	1460	1470	1480	1490	1500	1510
DEF4	TATGCAGGCCAGGCCTCCTGGCTTAAATATTCCCTCGGTCCAGGTAGTCAGCCT ::: :::: : :: : :: : :: : :: : :: :					
DEFX	TACACAG-CCAGGCTGTCCCAGTGGCTTCAATATTCTTTGGTCCAGATAGTCAGCCT 1470 1480 1490 1500 1510 1520					
	1520	1530	1540	1550	1560	1570
DEF4	CAGCCACCAGCATAGGTATCATGGGTCAATTGTCTTAGGAGTCATGAGGAATCCACAGT ::: :::: : :: : :: : :: : :: : :: :					
DEFX	CAGC-ACCAGTGTAGGCATCACAGGGTCAATTGTCTTAGGAGTCATGGAGAATTCATAGT 1530 1540 1550 1560 1570 1580					

Figure 2 (continued)

Figure 2 (continued)

10/16

2050 2060 2070 2080 2090 2100
DEF4 AACTCAAAAAGTTCCCTTCCAAACACACGTGTCCTACTTGACATGTCCAATAAGACGAT
::: :::::
DEFX AACTCAAGCAGTTCCCTTCCAAACACACATGTTCCTACTTAACGTGTCACAGAGATGAT
2050 2060 2070 2080 2090 2100

2110 2120 2130 2140
DEF4 CA---CAGCTTCT--TAAACATTAA-TTTTATTGTGAGAGAAGCCTCT-----
:: : : . :
DEFX CATACTCATANGCTGCTAAAACATTANTTTATTTGAGAAAAGTCTATTGTTCTTG
2110 2120 2130 2140 2150 2160

2150
DEF4 -----GCAG-----GTC---CTA---
::: :: : :::
DEFX GCCCATGGAGTTTCATTTNATTANTTTATTTATTTGCAGAGATGGAGTCTCACTATGT
2170 2180 2190 2200 2210 2220

2160
DEF4 -----GGTCT-----GTTTTTC-----
:::
DEFX TGCTCAAGCTGGTCTCCAACTCCTGGGCTCAAGCGATCTTCTACTTGGCCTTGAAAG
2230 2240 2250 2260 2270 2280

2170
DEF4 -----AATCAGGTT
::: :: : :::
DEFX CGCTGAGATTGCCTGTGAGCCATCATGGGGCTCACTGGCCCCTGATTAATCAGATT
2290 2300 2310 2320 2330 2340

2180 2190 2200 2210 2220 2230
DEF4 GTTTGTTTTTGCTATTGA-GTTGTTGACTTCCTTATGTATTCAAGATATTACCCCTTC
::
DEFX AATTGTTTTTGCTATTGAANTTGTGACTTCCTTGTATAATTGGATATTACCCATTG
2350 2360 2370 2380 2390 2400

2240 2250 2260 2270 2280 2290
DEF4 TACCACGTAGGCTTGCAAACATTTCTCTCATTTCTGGGTTGCCGTTCCCTCAGTTG
::
DEFX TAACACGTAGGTTGCAAATATTCTCTCATGTTCTGTGTTGCCCTTCACTCAGTTG
2410 2420 2430 2440 2450 2460

2300 2310 2320 2330 2340 2350
DEF4 ATTGTTCTTTGCTATGAAGATGCTTAGCGTTCAATGCAGCCCCGTTGTCTATTTC
::
DEFX ATGGTTCTTTGCTGTGCAGGTGCTTAGTGTCAACGCAGCCCCGTTGTCTATTTC
2470 2480 2490 2500 2510 2520

2360 2370 2380 2390 2400 2410
DEF4 CCATTTGTTTATTGCCTGTGCCTTGGTGTCAAGCCAAGAAATCATTACTCACGTCAAT
::
DEFX C-ATTT---TATTGCCTGTCCCTTGATGTCATAGCCAAGAAATAATTGCCAGATTAAT
2530 2540 2550 2560 2570 2580

Figure 2 (continued)

11/16

2420 2430 2440 2450 2460 2470
DEF4 GTCCAAA-GCTTTATCTTGATGTGCTTCTCGTAGTGTATGGTTTCAGGTCTTTCAA
::: :::: ::::: :: : :: : ::::: ::::: ::::: ::::: :::::
DEFX GTCAAAAGCTTTATCCCTATATATTCTCTAGTAGTT-TATGGTTTCAGATCTT-----
2590 2600 2610 2620 2630

2480 2490 2500 2510 2520 2530
DEF4 GTCTATGTTGAG-TCTTCAATCCATGTTGAGCTGATTCTT-TACATGTTGAGAGAAAG
::: :: : ::::: :: : ::::: :: : :: : :: : :::
DEFX ----ATGTTTAGGTCTCAATCCA--TTGAGTTGATTCTTGTATGTGGTATAAGAAAAAA
2640 2650 2660 2670 2680 2690

2540
DEF4 GACCACGTGTATGCACCT-----
::: :: : :: : :::
DEFX GACCACATGTATACATATCTCAAATTCTAAGGTAGTATATTAGACACATACAATGTGT
2700 2710 2720 2730 2740 2750

2550 2560 2570
DEF4 -----AGC---AACTCATGAAC-----CTTACA--CAACTCTT
::: :: : :: : :: : :: : :: : :: : :: : :::
DEFX CTATTTACACACATTGAGCTGAAAATAATAAACATATTTTATCTTCAATCAACTCTAT
2760 2770 2780 2790 2800 2810

2580 2590 2600 2610 2620 2630
DEF4 ATCTCTCTCACTGAGCTCATTTCACCTGTACCCGTATAAGGTCTTGTCCCTCTCACTCT
::: ::::: :: : ::::: :: : ::::: :: : :::
DEFX CTCTATCTCACTGAACCTGTTCACCTATAGCCTGATGAGGTTGCTGTCCCTCTACCCC
2820 2830 2840 2850 2860 2870

2640 2650 2660 2670 2680 2690
DEF4 GGGCCCTACAGGAGACTACTCACCCATTACCTCAGTCGCCCTCATGAGGGT-ATAAT
::: :: : :: : :: : :: : :: : :: : :: : :::
DEFX AGCTCCTATAGGAGACTGCTCATCCCCTAACCTCAAAAACCCCTCATGAGGGTGATAAT
2880 2890 2900 2910 2920 2930

2700 2710 2720 2730 2740 2750
DEF4 GACCTAGAACGCTGCAATGAGTTACT-CTCTACTCCACCGAATTCAAGGTCTGGCACCAG
::: :: : :: : :: : :: : :: : :: : :: : :::
DEFX GCCCTTGAATCCTGCAATGAATTAGTTCTACTACAGTGGAAATTCAAGGTCTGTTATGAG
2940 2950 2960 2970 2980 2990

2760 2770 2780 2790 2800 2810
DEF4 TGTTTAGACCT--GAAGAGAATAGTAGGGCCCATTATCAGGAAATAAGAGGCATTTGCTC
::: :: : :: : :: : :: : :: : :: : :: : :::
DEFX GGTCTGGATCTCTGAAGAGAAGAG--CTCTCATTTCAGAAAATAAGCAGGATTATTAC
3000 3010 3020 3030 3040

2820 2830 2840 2850 2860 2870
DEF4 TCTTAAATTATTGAATGAAAGCACTGTTCCATT-CTTTTAAATATTAAAGATTAAAC
::: :: : :: : :: : :: : :: : :: : :: : :::
DEFX CCTGAAATTACTGAATTAAATCACTGTTGATTACTTTGCAATATTAAA-----
3050 3060 3070 3080 3090

Figure 2 (continued)

12/16

	2880	2890	2900	2910	2920	2930
DEF4	CAGGAAATATTAGGTATTCCTGAAAACAGGAAAAATGCCAGGGCTCTCATCATCACCA					
DEFX	:: :::::: : : :::::: : :::::: : :::::: : :::::: : :::::: :					
	-AGTAAATATTTA--AACAGGTAAAAACAG-AAATAATGGTAGGGCTCTTATCATCACCG					
	3100	3110	3120	3130	3140	3150
	2940	2950	2960	2970	2980	
DEF4	TCAACTCACACCTAGGCACAGACACTAAACATAGAGCTTC---CTGTGAAGAAAGCTGGG					
DEFX	:: :: : :: : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::					
	TGAATTCCAAGCTAG-CATAGACACTAAACCTAGAGATTACACTAGAAATGAAAGCTGGG					
	3160	3170	3180	3190	3200	3210
	2990	3000	3010	3020	3030	3040
DEF4	AGAGCAGAGGAGGCATTCCAGGGATGTCAAGGCCAATAGGAGTCGGCATCCTCTCAAACA					
DEFX	:::::::::: : : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::					
	AGAGCAGAGGAGTC-TCAGAAGGATGTGGAGGCCAATGGACACCTGCAACCTCTCAAACG					
	3220	3230	3240	3250	3260	3270
	3050	3060	3070	3080	3090	3100
DEF4	AAATGCACACCTCCTCTCACTCAGAAGGCCAAGGTTCTTATCTGTGCTCTCCCCA					
DEFX	::::::: :::::::::: : :: :: :: :: :: :: :: :: :: :: :: :: :: ::					
	AAATGCCTACCTCCTCTCACT-----GC---AGCATCC--ATCTGTAGCCTCTCGCA					
	3280	3290		3300	3310	3320
	3110	3120	3130	3140	3150	3160
DEF4	GAA-AGCTATAAATCCAAGCTGGCTTCTCCCTCCCCACACAGCTGCTCTGCTCTCCCTC					
DEFX	:: ::::::: : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::					
	GCAGAGCTATAAATTCAAGCCTGGCTCCCTCCGTTCCCACACATCCACTCCTGCTCTCCCTC					
	3330	3340	3350	3360	3370	3380
	----- exon2 -----					
	3170	3180	3190	3200	3210	3220
DEF4	CTC----CAGGTACCCCCAGCCATGAGGATTATGCCCTCCTCGCTGCTATTCTCTTGG					
DEFX	:: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::					
	CTCTCCTCCAGGTGACTACAGTTATGAGGACCCCTCACCCCTCTCTGCTCTCCCTGG					
	3390	3400	3410	3420	3430	3440

	3230	3240	3250	3260	3270	3280
DEF4	TAGCCCTCCAGGTCCGGGGCAGGCCCACTCCAGGCAAGAGGTGATGAGGCTCCAGGCCAGG					
DEFX	:: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::					
	TGGCCCTTCAGGCCTGGGAGGCCGCTCCAGGCAAGAGCTCATGAGATGCCAGCCCAGA					
	3450	3460	3470	3480	3490	3500

	3290	3300	3310	3320	3330	3340
DEF4	AGCAGCGTGGGCCAGAAGACCAGGACATATCTATTCCCTTGCATGGGATAAAAGCTG					
DEFX	:: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::					
	AGCAGCCTCCAGCAGATGACCAGGATGTGGTCATTTACTTTCAAGGAGATGACAGCTG					
	3510	3520	3530	3540	3550	3560

Figure 2 (continued)

----->

	3350	3360	3370	3380	3390	3400
DEF4	CTCTTCAGGTTTCAGGTGAGAGAGGCCAGCATAAAAAGCTACCGAGTCTAGAGAGACGG					
	3570	3580	3590	3600	3610	
	3410	3420	3430	3440	3450	3460
DEF4	ATGGGAGATGGGCTCTGGAATCACATCTCAATGGTGGATGTCACTTAGGTGGCTTACTT					
	3620	3630	3640	3650	3660	3670
	3470	3480	3490	3500	3510	3520
DEF4	ACCATCTCTGGGCCTCGATTCTTATCTCGAAACTGAATAGAGAGACAAACAAATGTAA					
	3680	3690	3700	3710	3720	3730
	3530	3540	3550	3560	3570	3580
DEF4	GT-AGTCTTCTTCCTCAAAGACTTGATTCCAAGGTATGCTATAAAATCGCTAGGGTT					
	3740	3750	3760	3770	3780	3790
	3590	3600	3610	3620	3630	
DEF4	AAGATATGGAGAGACAGATTGACCAGTTCTGGATCTAAACAACTGA-GAT--ATTAT					
	3800	3810	3820	3830	3840	3850
	3640	3650	3660	3670	3680	3690
DEF4	AG-GGAAAATATTCATTCTGCCAACAAAGGAAATTAAAACTGGAGATGGCTTAAG					
	3860	3870	3880	3890	3900	3910
	3700	3710	3720	3730	3740	3750
DEF4	AGTATGTTCAAGGTGTGTCTGATGGGGCA--AAAGCACACAAATCAGAGCAAAAGAGAA					
	3920	3930	3940	3950	3960	3970
	3760	3770	3780	3790	3800	3810
DEF4	TGAGTCTCAAATCCTGTATGAGCAGCATTGCTCTGTGTATTTATTCTATTGACTAAGGT					
	3980	3990	4000	4010	4020	4030
	3820	3830	3840	3850	3860	3870
DEF4	TGTTTGTGCTACCGGCACTAATGCAGCCAGCATCACCAGTCAGCCAGCATGTGCATTCTC					
	4040	4050	4060	4070	4080	4090

Figure 2 (continued)

----- exon3 -----

DEF4	3880	3890	3900	3910	3920	3930
	CAAGATTCCCTTACCAACCACCGCTGACCTTGGTGCTTAATTCTCAGTCCTCCTCTGT					
DEFX	4100	4110	4120	4130	4140	4150
	CAAGATTCCCTTACCAACCACCGCTGNACCCGTAECTCAGTTCTGATGCTCTCTCTGG					

----- exon3 -----

DEF4	3940	3950	3960	3970	3980	3990
	GTTCCCAGGCTAACAAAGGGGCATGGTCTGCTTGCAGATTAGTATTCTGCCGGCGAAC					
DEFX	4160	4170	4180	4190	4200	4210
	GTCCCCAGGCTAACAAAGGGCTTGATCTGCCATTGCAGAGTACTATACTGCATTTTGG					

----- exon3 -----

DEF4	4000	4010	4020	4030	4040	4050
	AGAACTTCGTGTTGGGAAC TGCCCATGGTGGTGTGAGTTCACATACTGCTGCACGCG					
DEFX	4220	4230	4240	4250	4260	4270
	AGAACATCTGGTGGGACCTGCTTCATCCTTGGTGAACGCTACCCAATCTGCTGCT---					

----- exon3 -----

DEF4	4060	4070	4080	4090	4100	4110
	TGTCGATTAACATTCTGCTGTCAAAGAGAAATGTCATGCTGGAACGCCATCATCGGTGGT					
DEFX	-----ACTAA-----					

----- exon3 -----

DEF4	4120	4130	4140	4150	4160	4170
	GTTAGCTTCACATGCTTCTGCAGCTGAGCTTGAGAATAGAGAAAAATGAGCTCATAATT					
DEFX	4280	4290	4300			
	-----GCTTGAGACTAGAGAAAAA-GAGTTCATAATT					

----- exon3 -----

DEF4	4180	4190	4200	4210	4220	4230
	TGCTTTGAGAGCTACAGGAAATGGTTCTCCTATACTTTGTCCTAACATCTT-TCT					
DEFX	4310	4320	4330	4340	4350	4360
	TTCTTTGAGCATTAAGGAAATTGTTATT---CTTATACCTTGTCCCGATTTCTGTCC					

Poly Ad

----->

DEF4	4240	4250	4260	4270	4280	4290
	TGATCCTAAATATATCTCGAACAGATGTCCTTGTGTTACACCTTTGAAATTGAT					
DEFX	4370	4380	4390	4400	4410	
	TCATCCCAAATAAAACTTGGTAACATGATTCCGGGTTTTTTTTTT					

Figure 2 (continued)

	10	20	30	40	50	60
DEF4	GTCTGCCCTCTGCTCGCCCTGCCTAGCTTGAGGATCTGTACCCCCAGCCATGAGGATT					
DEFX	::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::					
	10	20	30	40	50	60
DEF4	CTCTGCCCACTCTGGTAGCCTCACGTAGCTAACAACTCTGTGACTACAGTTATGAGGACC					
DEFX						
	70	80	90	100	110	120
DEF4	ATCGCCCTCCTCGCTATTCTCTTGGTAGCCCTCCAGGTCCGGGCAGGCCACTCCAG					
DEFX	::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::					
	70	80	90	100	110	120
DEF4	CTCACCCCTCCTCTGCCTTCCTGGTGGCCCTCAGGCCTGGCAGAGCCGCTCCAG					
DEFX						
	130	140	150	160	170	180
DEF4	GCAAGAGGTGATGAGGCTCCAGGCCAGGAGCAGCGTGGGCCAGAAGACCAGGACATATCT					
DEFX	::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::					
	130	140	150	160	170	180
DEF4	GCAAGAGCTCATGAGATGCCAGCCAGAACAGCAGCCTCCAGCAGATGACCAGGATGTGGTC					
DEFX						
	190	200	210	220	230	240
DEF4	ATTTCCCTTGATGGATAAAAGCTCTGCTCTTCAGGTTCAAGGCTCAACAAGGGGCATG					
DEFX	::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::					
	190	200	210	220	230	240
DEF4	ATTTACTTTTCAGGAGATGACAGCTGCTCTTCAGGTTCCAGGCTCAACAAAGGGCTTG					
DEFX						
	250	260	270	280	290	300
DEF4	GTCTGCTCTTGAGATTAGTATTCTGCCGGCGAACAGAACCTCGTGGACTGCCTC					
DEFX	::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::					
	250	260	270	280	290	300
DEF4	ATCTGCCATTGCAGAGTACTATACTGCATTGGAGAACATCTGGTGGACCTGCTTC					
DEFX						
	310	320	330	340	350	360
DEF4	ATTGGTGGTGTGAGTTCACATACTGCTGCACCGTGTGATTAACGTTCTGCTGTCAA					
DEFX	::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::					
	310	320	330	340	350	360
DEF4	ATCCTTGGTGAACGCTACCCAACTGCTG-----CTACTAA-----					
DEFX						
	360	370	380	390	400	410
DEF4	370 380 390 400 410 420					
DEFX	-----					
	360	370	380	390	400	410
DEF4	GAGAATGTCATGCTGGAACGCCATCATCGTGGTAGCTTCACATGCTCTGCAGCT					
DEFX	-----					
	430	440	450	460	470	480
DEF4	GAGCTTGCAGAACATAGAGAAAAATGAGCTCATATTGCTTTGAGAGCTACAGGAAATGGT					
DEFX	::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::					
	400	410	420	430	440	450
DEF4	--GCTTGCAGACTAGAGAAAAA-GAGTCATAATTCTTCTTGAGCATTAAAGGGAAT--					
DEFX						
	490	500	510	520	530	
DEF4	TGTTTCTCCTATACTTTGTCTTAAACATCTT-TCTTGATCCTAAATATATATCTCGTAAC					
DEFX	::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::					
	460	470	480	490	500	510
DEF4	TGTTATTCTTATACTTGTCTCGATTTCTGTCCTCATCCAAATAACTTGGTAAC					
DEFX						
	540					
DEF4	AAG					
DEFX	::					
	540					
DEF4	ATG					
DEFX						

Figure 3

<----- Signal peptide -----><---
 5 10 15 20
 MetArgThrLeuThr LeuLeuSerAlaPhe LeuLeuValAlaLeu GlnAlaTrpAlaGlu

----- Propiece -----
 25 30 35 40
 ProLeuGlnAlaArg AlaHisGluMetPro AlaGlnLysGlnPro ProAlaAspAspGln

----- Propiece -----
 45 50 55 60
 AspValValIleTyr PheSerGlyAspAsp SerCysSerLeuGln ValProGlySerThr

><----- Mature peptide ----->
 65 70 75 80
 LysGlyLeuIleCys HisCysArgValLeu TyrCysIlePheGly GluHisLeuGlyGly

----- Mature peptide ----->
 85 90 94
 ThrCysPheIleLeu GlyGluArgTyrPro IleCysCysTyr

Figure 4

	SIGNAL	PROPIECE
DEF4_HUMAN	MRIIALLAAILLVALQVRA	GPLQAR-----GDEAPGQ-EQRGPEDQDISISFAWDKSS
DEF5_HUMAN	MRTIAILAAILLVALQQAQ	ESLQER-----ADEATTQ-KQSGEDNQDLAISFAGNGLS
DEF6_HUMAN	MRTLTIILTAVLLVALQAKA	EPLQAEDDPLQAKAYEADAQ-EQRGANDQDFAVSFAEDASS
DEF1_HUMAN	MRTLAILAAILLVALQQAQ	EPLQAR-----ADEVAAAPEQIAADIPEVVVS LAWDES
DEFX	MRTLTLSSAFLVALQAWA	EPLQAR-----AHMPAQ-KQPPADDQDVVIYFSGDDSC
	** . . * . * ***** * **	* *

	PROPIECE	Mature PEPTIDE
DEF4_HUMAN	ALQVSGSTRGM	VCSCRLVFCRRTELRVGNCLIGGVSFYCCTRVD
DEF5_HUMAN	ALRTSGSQARA	TCYCRTGRCATRESLSGVCEISGRLYRLCCR--
DEF6_HUMAN	SLRALGSTRAF	TCHCRR-SCYSTEYSYGTCTVMGINHRFCCL--
DEF1_HUMAN	APKHPGSRKNM	ACYCRIPACIAGERRYGTIYQGRLWAFCC---
DEFX	SLQVPGSTKGL	ICHCRVLYCIFGEHLGGTCFILGERYPICCY---
	. ** * *** * * * * * **	^ ^ ^ ^ ^ ^ ^ ^

Figure 5